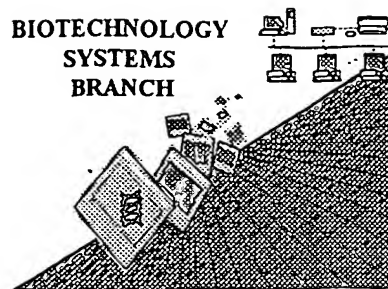BIOTECHNOLOGY
SYSTEMS
BRANCH

RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information
Center (STIC) detected errors when processing the following computer readable
form:

Application Serial Number: *10/023,909*
Source: *DIPE*
Date Processed by STIC: *1/16/2002*

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE
   APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A
   NOTICE TO COMPLY
FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER
VERSION 3.1 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND
TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:
      http://www.uspto.gov/web/offices/pac/checker

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is
a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.
Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom, including:
1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm> , EFS Submission
   User Manual - ePAVE)
2. U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202
3. Hand Carry directly to:
   U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7th Floor, Examiner Name,
   Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202
          Or
   U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two,
   2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office,
   Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Raw Sequence Listing Error Summary

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: _10/023,909_

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1____Wrapped Nucleics
Wrapped Aminos
The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2____Invalid Line Length
The rules require that a line not exceed 72 characters in length. This includes white spaces.

3____Misaligned Amino
Numbering
The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

4____Non-ASCII
The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

5____Variable Length
Sequence(s)____contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6____PatentIn 2.0
"bug"
A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**

7____Skipped Sequences
(OLD RULES)
Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i)   SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8____Skipped Sequences
(NEW RULES)
Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

9____Use of n's or Xaa's
(NEW RULES)
Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa; and which residue n or Xaa represents.

10____Invalid <213>
Response
Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence _(and more)_

11____Use of <220>
Sequence(s) _1-27 (and more)_ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32)   (Sec. 1.823 of Sequence Rules)

12____PatentIn 2.0
"bug"
Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13____Misuse of n
n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

AMC/MH – Biotechnology Systems Branch – 08/21/2001

OIPE

RAW SEQUENCE LISTING   DATE: 01/16/2002
PATENT APPLICATION: US/10/023,909   TIME: 18:30:53

Input Set : A:\C1039-7058.txt
Output Set: N:\CRF3\01162002\J023909.raw

```
 3 <110> APPLICANT: Davis, Heather L.
 4        Schorr, Joachim
 5        Krieg, Arthur M.
 7 <120> TITLE OF INVENTION: Use of Nucleic Acids Containing
 8        Unmethylated CpG Dinucleotide as an Adjuvant
10 <130> FILE REFERENCE: C1039/7058/HCL
12 <140> CURRENT APPLICATION NUMBER: US/10/023,909
13 <141> CURRENT FILING DATE: 2001-12-18
15 <150> PRIOR APPLICATION NUMBER: US 09/325,193
16 <151> PRIOR FILING DATE: 1999-06-03
18 <150> PRIOR APPLICATION NUMBER: US 09/154,614
19 <151> PRIOR FILING DATE: 1998-09-16
21 <150> PRIOR APPLICATION NUMBER: PCT/US98/04703
22 <151> PRIOR FILING DATE: 1998-03-10
24 <150> PRIOR APPLICATION NUMBER: US 60/040,376
25 <151> PRIOR FILING DATE: 1997-03-10
27 <160> NUMBER OF SEQ ID NOS: 98
29 <170> SOFTWARE: FastSEQ for Windows Version 3.0
31 <210> SEQ ID NO: 1
32 <211> LENGTH: 15
33 <212> TYPE: DNA
34 <213> ORGANISM: Artificial Sequence
36 <220> FEATURE:
36 <223> OTHER INFORMATION:
36 <400> SEQUENCE: 1
37  gctagacgtt agcgt                                     15
39 <210> SEQ ID NO: 2
40 <211> LENGTH: 15
41 <212> TYPE: DNA
42 <213> ORGANISM: Artificial Sequence
44 <220> FEATURE:
44 <223> OTHER INFORMATION:
44 <400> SEQUENCE: 2
45  gctagatgtt agcgt                                     15
47 <210> SEQ ID NO: 3
48 <211> LENGTH: 15
49 <212> TYPE: DNA
50 <213> ORGANISM: Artificial Sequence
52 <220> FEATURE:
53 <221> NAME/KEY: modified_base
54 <222> LOCATION: (7)...(7)
55 <223> OTHER INFORMATION: m5c
57 <400> SEQUENCE: 3
58  gctagacgtt agcgt                                     15
60 <210> SEQ ID NO: 4
61 <211> LENGTH: 15
62 <212> TYPE: DNA
```

Does Not Comply
Corrected Diskette Needed

pp 1-5

(global error)
→ see item 11 on Error Summary Sheet

W-->
W-->
W-->
W-->

Input Set : A:\C1039-7058.txt
Output Set: N:\CRF3\01162002\J023909.raw

```
 63 <213> ORGANISM: Artificial Sequence
 65 <220> FEATURE:
 66 <221> NAME/KEY: modified_base
 67 <222> LOCATION: (13)...(13)
 68 <223> OTHER INFORMATION: m5c
 70 <400> SEQUENCE: 4
 71  gctagacgtt agcgt                                    15
 73 <210> SEQ ID NO: 5
 74 <211> LENGTH: 15
 75 <212> TYPE: DNA
 76 <213> ORGANISM: Artificial Sequence
 78 <220> FEATURE:
 78 <223> OTHER INFORMATION:
 78 <400> SEQUENCE: 5
 79  gcatgacgtt gagct                                    15
 81 <210> SEQ ID NO: 6
 82 <211> LENGTH: 20
 83 <212> TYPE: DNA
 84 <213> ORGANISM: Artificial Sequence
 86 <220> FEATURE:
 86 <223> OTHER INFORMATION:
 86 <400> SEQUENCE: 6
 87  atggaaggtc cagcgttctc                               20
 89 <210> SEQ ID NO: 7
 90 <211> LENGTH: 20
 91 <212> TYPE: DNA
 92 <213> ORGANISM: Artificial Sequence
 94 <220> FEATURE:
 94 <223> OTHER INFORMATION:
 94 <400> SEQUENCE: 7
 95  atcgactctc gagcgttctc                               20
 97 <210> SEQ ID NO: 8
 98 <211> LENGTH: 20
 99 <212> TYPE: DNA
100 <213> ORGANISM: Artificial Sequence
102 <220> FEATURE:
103 <221> NAME/KEY: modified_base
104 <222> LOCATION: (3)...(3)
105 <223> OTHER INFORMATION: m5c
107 <400> SEQUENCE: 8
108  atcgactctc gagcgttctc                               20
110 <210> SEQ ID NO: 9
111 <211> LENGTH: 20
112 <212> TYPE: DNA
113 <213> ORGANISM: Artificial Sequence
115 <220> FEATURE:
116 <221> NAME/KEY: modified_base
117 <222> LOCATION: (18)...(18)
118 <223> OTHER INFORMATION: m5c
```

W--> 78
W--> 78
W--> 86
W--> 86
W--> 94
W--> 94

```
    120 <400> SEQUENCE: 9
    121  atcgactctc gagcgttctc                                      20
    123 <210> SEQ ID NO: 10
    124 <211> LENGTH: 20
    125 <212> TYPE: DNA
    126 <213> ORGANISM: Artificial Sequence
W--> 128 <220> FEATURE:
W--> 128 <223> OTHER INFORMATION:
    128 <400> SEQUENCE: 10
    129  atggaaggtc caacgttctc                                      20
    131 <210> SEQ ID NO: 11
    132 <211> LENGTH: 20
    133 <212> TYPE: DNA
    134 <213> ORGANISM: Artificial Sequence
W--> 136 <220> FEATURE:
W--> 136 <223> OTHER INFORMATION:
    136 <400> SEQUENCE: 11
    137  gagaacgctg gaccttccat                                      20
    139 <210> SEQ ID NO: 12
    140 <211> LENGTH: 20
    141 <212> TYPE: DNA
    142 <213> ORGANISM: Artificial Sequence
W--> 144 <220> FEATURE:
W--> 144 <223> OTHER INFORMATION:
    144 <400> SEQUENCE: 12
    145  gagaacgctc gaccttccat                                      20
    147 <210> SEQ ID NO: 13
    148 <211> LENGTH: 20
    149 <212> TYPE: DNA
    150 <213> ORGANISM: Artificial Sequence
W--> 152 <220> FEATURE:
W--> 152 <223> OTHER INFORMATION:
    152 <400> SEQUENCE: 13
    153  gagaacgctc gaccttcgat                                      20
    155 <210> SEQ ID NO: 14
    156 <211> LENGTH: 20
    157 <212> TYPE: DNA
    158 <213> ORGANISM: Artificial Sequence
    160 <220> FEATURE:
    161 <221> NAME/KEY: modified_base
    162 <222> LOCATION: (14)...(14)
    163 <223> OTHER INFORMATION: m5c
    165 <400> SEQUENCE: 14
    166  gagaacgctg gaccttccat                                      20
    168 <210> SEQ ID NO: 15
    169 <211> LENGTH: 20
    170 <212> TYPE: DNA
    171 <213> ORGANISM: Artificial Sequence
W--> 173 <220> FEATURE:
```

```
              RAW SEQUENCE LISTING              DATE: 01/16/2002
              PATENT APPLICATION:  US/10/023,909  TIME: 18:30:53

              Input Set : A:\C1039-7058.txt
              Output Set: N:\CRF3\01162002\J023909.raw

W--> 172 <223> OTHER INFORMATION:
     173 <400> SEQUENCE: 15
     174  gagaacgatg gaccttccat                                    20
     176 <210> SEQ ID NO: 16
     177 <211> LENGTH: 20
     178 <212> TYPE: DNA
     179 <213> ORGANISM: Artificial Sequence
W--> 181 <220> FEATURE:
W--> 181 <223> OTHER INFORMATION:
     181 <400> SEQUENCE: 16
     182  gagaacgctc cagcactgat                                    20
     184 <210> SEQ ID NO: 17
     185 <211> LENGTH: 20
     186 <212> TYPE: DNA
     187 <213> ORGANISM: Artificial Sequence
W--> 189 <220> FEATURE:
W--> 189 <223> OTHER INFORMATION:
     189 <400> SEQUENCE: 17
     190  tccatgtcgg tcctgatgct                                    20
     192 <210> SEQ ID NO: 18
     193 <211> LENGTH: 20
     194 <212> TYPE: DNA
     195 <213> ORGANISM: Artificial Sequence
     197 <220> FEATURE:
     198 <221> NAME/KEY: modified_base
     199 <222> LOCATION: (12)...(12)
     200 <223> OTHER INFORMATION: m5c
     202 <400> SEQUENCE: 18
     203  tccatgtcgg tcctgatgct                                    20
     205 <210> SEQ ID NO: 19
     206 <211> LENGTH: 20
     207 <212> TYPE: DNA
     208 <213> ORGANISM: Artificial Sequence
W--> 210 <220> FEATURE:
W--> 210 <223> OTHER INFORMATION:
     210 <400> SEQUENCE: 19
     211  tccatgacgt tcctgatgct                                    20
     213 <210> SEQ ID NO: 20
     214 <211> LENGTH: 20
     215 <212> TYPE: DNA
     216 <213> ORGANISM: Artificial Sequence
W--> 218 <220> FEATURE:
W--> 218 <223> OTHER INFORMATION:
     218 <400> SEQUENCE: 20
     219  tccatgtcgg tcctgctgat                                    20
     221 <210> SEQ ID NO: 21
     222 <211> LENGTH: 8
     223 <212> TYPE: DNA
     224 <213> ORGANISM: Artificial Sequence
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RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/023,909

DATE: 01/16/2002
TIME: 18:30:53

Input Set : A:\C1039-7058.txt
Output Set: N:\CRF3\01162002\J023909.raw

```
W--> 226  <220> FEATURE:
W--> 226  <223> OTHER INFORMATION:
     226  <400> SEQUENCE: 21
     227  tcaacgtt                                                      8
     229  <210> SEQ ID NO: 22
     230  <211> LENGTH: 8
     231  <212> TYPE: DNA
     232  <213> ORGANISM: Artificial Sequence
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     234  <400> SEQUENCE: 22
     235  tcagcgct                                                      8
     237  <210> SEQ ID NO: 23
     238  <211> LENGTH: 8
     239  <212> TYPE: DNA
     240  <213> ORGANISM: Artificial Sequence
W--> 242  <220> FEATURE:
W--> 242  <223> OTHER INFORMATION:
     242  <400> SEQUENCE: 23
     243  tcatcgat                                                      8
     245  <210> SEQ ID NO: 24
     246  <211> LENGTH: 8
     247  <212> TYPE: DNA
     248  <213> ORGANISM: Artificial Sequence
W--> 250  <220> FEATURE:
W--> 250  <223> OTHER INFORMATION:
     250  <400> SEQUENCE: 24
     251  tcttcgaa                                                      8
     253  <210> SEQ ID NO: 25
     254  <211> LENGTH: 7
     255  <212> TYPE: DNA
     256  <213> ORGANISM: Artificial Sequence
W--> 258  <220> FEATURE:
W--> 258  <223> OTHER INFORMATION:
     258  <400> SEQUENCE: 25
     259  caacgtt                                                       7
     261  <210> SEQ ID NO: 26
     262  <211> LENGTH: 8
     263  <212> TYPE: DNA
     264  <213> ORGANISM: Artificial Sequence
W--> 266  <220> FEATURE:
W--> 266  <223> OTHER INFORMATION:
     266  <400> SEQUENCE: 26
     267  ccaacgtt                                                      8
     269  <210> SEQ ID NO: 27
     270  <211> LENGTH: 8
     271  <212> TYPE: DNA
     272  <213> ORGANISM: Artificial Sequence
W--> 274  <220> FEATURE:
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The types of errors shown exist throughout
the Sequence Listing. Please check subsequent
sequences for similar errors.

```
                    VERIFICATION SUMMARY            DATE: 01/16/2002
                    PATENT APPLICATION:  US/10/023,909    TIME: 18:30:54

                    Input Set : A:\C1039-7058.txt
                    Output Set: N:\CRF3\01162002\J023909.raw

L:12 M:270 C: Current Application Number differs, Replaced Application Number
L:36 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:36 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:44 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:44 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
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L:266 M:258 W: Mandatory Feature missing, <220> FEATURE:
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L:297 M:258 W: Mandatory Feature missing, <220> FEATURE:
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```
                 VERIFICATION SUMMARY              DATE: 01/16/2002
                 PATENT APPLICATION:  US/10/023,909   TIME: 18:30:54

                 Input Set : A:\C1039-7058.txt
                 Output Set: N:\CRF3\01162002\J023909.raw

L:297 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
L:305 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:305 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION:
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